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<120> NOVEL CHEMOKINE-LIKE POLYPEPTIDES

<130> WO582

<160> 52

<170> PatentIn version 3.0

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Lys Ile Tyr Lys His Ala Asp Thr Leu Phe Tyr Ile Tyr Ile Pro Ile
20 25 30

Tyr Val Cys Met Cys Ile His Ser Tyr Ala Leu Tyr Asn Ser Ile Leu
35 40 45

Val Ser Asp Gly Leu Arg Met Leu Arg Cys Ser His Lys Ile Ile Ile
50 55 60

Ser Thr Leu Thr Ile Thr Phe Leu Cys Leu His Ala Glu Ile Leu Thr
65 70 75 80

Asn Gly Leu Gln Leu Pro Thr Val Phe Ser Thr Pro Ala Cys Cys Thr
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Gly Trp

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gacaaagatg gcactgagac tatgtgtgta gctggaagca acctaaatgt ccattcgtgg 240

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Met Val Ile Pro His Leu Val Leu Leu Thr Leu Ile Ser Phe Arg Leu
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20 25 30

Leu Cys Leu Cys Asp Ser Gly Arg Ile Pro Ala Arg Asn Ala Leu Asp
35 40 45

Pro Ser Gln Asp Gln Gln Pro Leu Gln Gln Asp Lys Asp Gly Thr Glu
50 55 60

Thr Met Cys Val Ala Gly Ser Asn Leu Asn Val His Ser Trp Val Asn
65 70 75 80

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85 90 95

Arg Lys Leu Cys Arg Leu Leu Gln Gln Arg
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Asp Ser Leu Gln Phe Tyr Met Asn Phe Glu Ser Val Cys Arg Cys Leu

20 25 30

Gln Lys Ile Ser Val Ile Leu Ile Gly Ile Ala Phe Asn Leu Cys Asn
35 40 45

Asp Leu Gly Ser Ile Val Ile Leu Thr Val Leu Cys Ile Leu Ile His
50 55 60

Glu Tyr Glu Ile Tyr Phe Leu Leu Phe Arg Ser Leu Ile Phe Ser Leu
65 70 75 80

Cys Phe Ile Val Pro Glu Tyr Ser Lys Phe Cys Asn Phe Tyr Val Lys
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Phe Ile Leu Lys Asn Leu Phe Leu Met Leu Ser
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20 25 30

Glu Val Asp Leu Asn Gln His Pro Val Arg Cys Cys Tyr Ser Phe Pro
35 40 45

Thr Phe Cys Val Glu Gly Met Leu Leu Lys Leu Cys Phe Asn Met Glu
50 55 60

Pro His Cys Phe Leu Ser Leu Thr Gln Ser Thr Val Ser Leu Ser Gln
65 70 75 80

Gly Cys His Leu Phe Ser Val Phe Val Gln Leu Ile Trp Thr Ala His
85 90 95

Leu Asp Arg His Lys Glu
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cctatgattg tagagctaaa gcaaaaatgt gaaatgtttt gtcagaaata tctagttgat 180

aaagattatt cctttcgtgt ttctgtaacc tgtcagttct ttatactttt acatgattcc 240

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20 25 30

Ser Phe Lys Gln Glu Val Pro Met Ile Val Glu Leu Lys Gln Lys Cys
35 40 45

Glu Met Phe Cys Gln Lys Tyr Leu Val Asp Lys Asp Tyr Ser Phe Arg
50 55 60

Th s Gln Phe Phe Ile Leu Leu His Asp
65 70 75 80

Thr Glu Asn Thr Trp Ser Thr Ile Pro Thr Leu Ser Ala Leu Ile Ser
85 90 95

Ser Leu Ile Phe Leu
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gctctgagcc tcggcgctgc tggcatttgg ggctggatga ctctttgctg tggctgctgt 120

cctgtgcatt acaggacatt acgtagcatc cctgaccaca acctactaga tgccagtagc 180

acccccctccc tagttatgac aaccagaaac atctccagac attgccaatg tcccctggtg 240

gcaaaatcat ccccggctga gaatgagtgt tgcacggtaa ttcctccatt ccaaattaac 300

agagcactta ggaacgagtg ctttctccta ttactttccc tttaa 345

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<400> 12

Gly Leu Leu Ile Lys Ala Leu Tyr Leu Ala Ser Al
1 5 10 15

Ala Gly Ala Leu Ser Leu Gly Ala Ala Gly Ile Trp Gly Trp Met Thr
20 25 30

Leu Cys Cys Gly Cys Cys Pro Val His Tyr Arg Thr Leu Arg Ser Ile
35 40 45

Pro Asp His Asn Leu Leu Asp Ala Ser Ser Thr Pro Ser Leu Val Met
50 55 60

Thr Thr Arg Asn Ile Ser Arg His Cys Gln Cys Pro Leu Val Ala Lys
65 70 75 80

Ser Ser Pro Ala Glu Asn Glu Cys Cys Thr Val Ile Pro Pro Phe Gln
85 90 95

Ile Asn Arg Ala Leu Arg Asn Glu Cys Phe Leu Leu Leu Leu Ser Leu
100 105 110

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atggactatt gtgatgaatg cactctgcag ggtgtgttcc cagagcacag aagtaaccag 180

gc igtgtt gcccacacca aaacactgca gactta

gtgctgtcag agtgtccatt tcaagctccc tgttggccac agacaaaagc cattatccta 300

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aaatgcacaa ttttgttaga atttttctga 390

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Met Asp Ser Arg Phe Gln Leu Lys Leu Leu Phe His Cys Phe Gln Gly
20 25 30

Leu Phe Gln Arg Ser His Met Asp Tyr Cys Asp Glu Cys Thr Leu Gln
35 40 45

Gly Val Phe Pro Glu His Arg Ser Asn Gln Arg Ala Ala Arg Glu Val
50 55 60

Leu Pro Thr Pro Lys His Cys Arg Leu Ile Pro Leu Gly Thr Val Leu
65 70 75 80

Ser Glu Cys Pro Phe Gln Ala Pro Cys Trp Pro Gln Thr Lys Ala Ile
85 90 95

Le Trp Arg Asn Leu Glu Val Leu Glu Val Al
100 105 110

Leu Arg Gln Asp Cys Phe Lys Cys Thr Ile Leu Leu Glu Phe Phe
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gcagcagggc acgcacagcc ctgttttctc atctgctttc agcagcattt gcctcctact 120

ccacttgggt cactcaaggg tcccaaaata gacctgtgca ttcatgggac ccctcccacc 180

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Gln His Leu Pro Pro Thr Pro Leu Gly Ser Leu Lys Gly Pro Lys Ile
35 40 45

Asp Leu Cys Ile His Gly Thr Pro Pro Thr Cys Leu Ser Ala Gln Cys
50 55 60

Leu Cys Trp Asp Arg Gln Gln Val Leu Lys Ser Gln Pro Leu Leu Pro
65 70 75 80

Ala Gly Val His Leu Arg Thr Phe Pro Ala Ile
85 90

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<210> 18
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<400> 18
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<400> 19
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<400> 20
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<211> 21
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<400> 26
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<400> 33
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<210> 38

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<400> 38
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<400> 40
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<210> 41
<211> 57
<212> DNA
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<400> 41
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<210> 42
<211> 68
<212> DNA
<213> synthetic construct

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acagcatg 68

<210> 43
<211> 62
<212> DNA
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gc 62

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<211> 73
<212> DNA
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gaaagttctc agg 73

<211> 59

<212> DNA

<213> synthetic construct

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<211> 69

<212> DNA

<213> synthetic construct

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taataggag 69

<210> 47

<211> 59

<212> DNA

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taacaaaatt g 71

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<210> 50
<211> 69
<212> DNA
<213> synthetic construct

<400> 50

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cagcaaacg 69

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<212> DNA
<213> synthetic construct

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<211> 68

<212> DNA

<213> synthetic construct

<400> 52

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caaagagg 68